

WHAT IS CLAIMED IS:

1. A method for providing genomic and proteomic research products and services, comprising the steps of:

providing a customer with access to a genomic and proteomic research products and services database;

enabling the customer to access at least one of a clone collection database associated with the genomic and proteomic research products and services database and an expression database associated with the genomic and proteomic research products and services database;

providing the customer with selected genomic and proteomic research products and services; and

providing the customer with additional genomic and proteomic research products related to the selected genomic and proteomic research products and services.

2. The method of claim 1, wherein the clone collection database is divided into a private area and a public area, and further wherein the clone collection database contains information identifying the characteristics of individual members of a clone collection.

3. The method of claim 1, wherein the expression database contains information identifying optimized expression sequences for one or more clones in the clone collection.

4. The method of claim 1, further comprising the step of assembling a subscriber record, wherein the assembling step comprises the steps of:

providing a subscription identification field in the subscriber record;

providing a subscription fee payment field in the subscriber record;

providing a clone purchase credit field in the subscriber record;

providing a clone purchase field in the subscriber record; and

providing a subscriber site identification field in the subscriber record.

5. The method of claim 1, further comprising the steps of designating one or more of the customers as subscribers and enabling the subscribers to identify clones to be built and added to the clone collection.

6. The method of claim 5, further comprising the step of enabling the subscribers to prioritize the order in which the identified clones are built and added to the clone collection.

7. The method of claim 6, further comprising the step of updating the clone collection database once the identified clones have been built and added to the clone collection.

8. The method of claim 5, further comprising the step of providing research and development consulting services to one or more sites designated by the subscriber.

9. A method for providing geneomic and proteomic research products and services, comprising the steps of:

(1) enabling customers to select genomic and proteomic research products and services to be provided;

(2) providing the selected genomic and proteomic research products and services to the customers;

(3) identifying additional genomic and proteomic research products and services that are related to the selected genomic and proteomic research products and services; and

(4) providing the additional genomic and proteomic research products and services.

10. The method of claim 9, wherein step (1) comprises the step of providing the customers with access to a clone collection database containing information describing clone collections organized according to gene families.

11. The method of claim 10, wherein step (1) comprises the step of enabling the customers to identify a gene of interest

12. The method of claim 11, wherein step (4) comprises the step of identifying additional members of the gene family associated with the gene of interest.

13. The method of claim 11, wherein step (4) comprises the step of producing antibodies to additional members of the gene family associated with the gene of interest.

14. The method of claim 11, wherein step (4) comprises the step of providing reagents that are specific to the gene of interest.

15. A method for providing genomic and proteomic research products and services, comprising the steps of:

- providing a subscriber with access to a genomic and proteomic research products and services database;

- enabling the subscriber to access at least one of a clone collection database and an expression database associated with the genomic and proteomic research products and services database, wherein the clone collection database has a private area and a public area, and further wherein the clone collection database contains information identifying the characteristics of a clone collection and wherein the expression database contains information identifying optimized expression sequences for one or more clones in the clone collection; and

- assembling a subscriber record for the subscriber.

16. The method of claim 15, wherein the assembling step comprises the steps of:

- providing a subscription identification field in the subscriber record;

providing a subscription fee payment field in the subscriber record;
providing a clone purchase credit field in the subscriber record;
providing a clone purchase field in the subscriber record; and
providing a subscriber site identification field in the subscriber record.

17. The method of claim 15, further comprising the step of enabling the subscriber to identify clones to be built and added to the clone collection.

18. The method of claim 17, further comprising the step of enabling the subscriber to prioritize the order in which the identified clones are built and added to the clone collection.

19. The method of claim 18, further comprising the step of updating the clone collection database once the identified clones have been built and added to the clone collection.

20. The method of claim 15, further comprising the step of providing research and development consulting services to one or more sites designated by the subscriber.

21. The method of claim 15, further comprising the step of dividing the private area of the clone collection database into separate areas, each separate area being accessible by a specific subscriber.

22. A system for providing genomic and proteomic research products and services, comprising:

one or more databases accessible by a subscriber; and

a provider of genomic and proteomic research products and services, wherein the provider provides selected genomic and proteomic research products and services to the subscriber, and

further wherein the provider provides additional genomic and proteomic research products and services related to the selected genomic and proteomic research products and services.

23. The system of claim 22, wherein one of the databases is a clone collection database having a private area and a public area, and further wherein the clone collection database contains information identifying the characteristics of individual members of a clone collection.

24. The system of claim 23, wherein one of the databases is an expression database, wherein the expression database contains information identifying optimized expression sequences for one or more clones in the clone collection.

25. The system of claim 23, wherein the subscriber is able to identify clones to be built and added to the clone collection.

26. The system of claim 25, wherein the subscriber is able to prioritize the order in which the identified clones are built and added to the clone collection.

27. The system of claim 26, wherein the clone collection database is capable of being updated once the identified clones have been built and added to the clone collection.

28. The system of claim 22, further comprising a subscriber record including a subscription identification field, a subscription fee payment field, a clone purchase credit field, a clone purchase field, and a subscriber site identification field.

29. The system of claim 22, further comprising one or more sites designated by the subscriber to receive research and development consulting services from the provider.

30. A method of making a collection of clones, comprising:
obtaining from a customer information of a type of polypeptide in which the customer is interested; and
compiling a collection of clones comprising ORFs encoding the type of polypeptide in which the customer is interested.
31. A method according to claim 30, wherein the type of polypeptide is a druggable target.
32. A method according to claim 30, wherein the type of polypeptide is selected from the group consisting of kinases, phosphatases, G-protein-coupled receptors, ion channels, proteases, nuclear receptors, secretory proteins, growth factors, cytokines, chemokines, membrane transporters, chemokine receptors, and integrins.
33. A method according to claim 30, wherein the collection comprises a gene family.
34. A method according to claim 33, wherein the gene family comprises proteins related in amino acid sequence and/or splice variants of the same gene.
35. A method according to claim 30, wherein one or more clones in the collection comprise an open reading frame flanked by a first and a second recombination site, wherein the first and second recombination sites do not recombine with each other.
36. A method according to claim 30, wherein compiling comprises:
obtaining a nucleotide sequence of interest from the customer;
comparing the nucleotide sequence of interest to nucleotide sequences in a database to identify a nucleic acid molecule comprising all or a portion of nucleotide sequence of interest; and

amplifying all or a portion of the nucleic acid molecule.

37. A clone collection, comprising:

a plurality of clones, each clone comprising a nucleic acid sequence of interest, wherein the nucleic acid sequences of interest encode all or substantially all known polypeptides having a specified activity.

38. The clone collection of claim 37, wherein the specified activity is an enzymatic activity.

39. The clone collection of claim 38, wherein the activity is a kinase activity.

40. The clone collection of claim 37, wherein the activity is a G-protein-coupled receptor activity.

41. The clone collection of claim 37, wherein the nucleic acid sequences of interest comprise suppressible stop codons.

42. The clone collection of claim 37, wherein the nucleic acid sequences of interest comprise a tag sequence and a suppressible stop codon located between the tag sequence and the encoded polypeptide.

43. The clone collection of claim 37, wherein the nucleic acid sequences of interest are flanked by a first and a second recombination site and the first and the second recombination sites do not recombine with each other.